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#### Amendments to the Specification:

Please replace Table 1, beginning on page 8, line 10, with the following amended Table

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Marker Name	Sequence	SEQ ID NO
1-85/5B5/86-1	AGCAAGCTTACATGCGTGGA [GT/AA] GAGAGTCCTCGAGATCAACC	30
2-85/5B12/N3-1	CCTTGATCTCTAAGTAATC [A/G] TCTCACCGGAAGATCCCTGA	31
3-85/5C3/86-2	ACCATCCATTAAACTGTATC[A/G]TCGCAATCTAACCAAAAGTT	32
4-85/5E1/86-1	TAAAGCAAAGAGAGTCTTAC [C/A] GTCTGCTGCATGATATACCC	33
5-85/5E1/86-2	CTACTGATAGTGAACCACCC[A/C]ATCCCCAAATTTAAAGCAAA	.34
6-85/6A11/86	ATCCTATTGGTAGTAACACA [G/A] ATTGAGTTAATGTTGCAGGG	35
7-N1/6A11/N2	AGGCAAAGCGGTAGTTGCAA [G/A] ACTGCTTCTCACGAGGTAAT	36
8-N1/6A9/N2-1	CCAGCTTCAATGTCTGCATG[C/A]TTGTGTCGATGCCAAAGTTC	37
9-N1/6A9/N2-2	AAAGTTCATTACGATGATCT [A/G] ACCCTGCAGTCATCCATGGA	38
10-85/6A12/86	CTTCCCCCCCTCAATACCTC [T/G] TTCAAAAGTGAAAAGTGCAG	39
11-N1/6D1/N2-1	ATTTTGTTTTGTTTCTTGTC [G/C] GGTCAGGTCAGAACAAAGTT	40
12-N1/6H5/N2	AAACCAGAGCCACCTCCTTA[C/]CCACCTCATCGTTTCCTTTC	41
13-86/6F11/N2-2	GATTTCGACCGCAGTCTCAC [G/T] GAGGATGAGTATATCGCTTT	42
14-N1/6F11/N2	TAGGACAGGCAAACAATCTA [C/A] GCGGTCAAAATCCGATTTCG	43
16-N1/8B5/N2	ACTCAAAAAACGATACCTC [G/C] GCCGTCTCGCCGTCTCGC	44
17-N1/8D4/N2-1	CAGGAGACAGTTACAGTCCC [/A] CAGAGTCGCAAGGATCTCGAA	45
18-85/8D4/86-2	CTGATCTTGAAGGAGACC [A/G] CCACAAGGTTCCATCCTATG	46
19-85/8H11/86	AGTGCGAGGCTCAGTTGGAT [G/T] ATTAGGGTGTCAGTAAATCA	47
20-85/10B8/86	NAGGTCCATGATGATGACAA [T/A] AAAGGTATTCCACATGTCAA	48
21-N2/10B8/N3-2	ACATCCAACTTTCTCCAGT[T/C]CTTTATTCTATCCTGATTTG	49
21 N2/10B8/N3 2	ACATCCAACTTTTCTCCAGT[T/C]CTTTATTCTATCCTGATTTG	99
22-N2/10B8/N3-1	AAGGTATTCCATTGGTATAC [A/C] TCCAACTTTTCTCCAGTTCT	<u>505+</u>

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<u>5657</u> <u>57</u>58 5960 6162 6263 6364 6465 9939 <del>29</del>999 6768 6869 0269 707 7172 7273 <u>5253</u> 5455 <u>55</u>56 5859 6061 GACCTTCTTGGGAAAGAAG [T/C] TGTAACCGCGTCGAGATTCG GGAATTCAATACTCGCCAAC [G/T] TCTTCATTGCTGTCGTCGGC AACTTGGAATTCCACAACTT [G/C] AGAAACTTCGATGTGGTGCC GTCAAAAGCCACGGATTCAA [G/A] AACGTGCTCTTCTTGCGCCT AANACCCTGAGCTCATGCCT [C/T] TGACCCATGTTCTTGCCACC TTTGGGACCGTTGGAGTTGC [A/G] TCTGCGGCTATGACGGTGGA GCTGCTCTAGGGATGCTCAG [C/T] ACCATCGCCACCGGTTTGGC ATAGAAACCGCCGATGCTCA [A] GGACACGCCACCGTCTTCGT GAGAAAGTGCTTGTGGAGAT [C/T] TACAAGTCCATACTGATGGC TCCTTACGCCTTCAAGCGCA [C/G] CGGCTGGCTCATGGGTGTCC TGTATCTATGCGGTGGCTGC [G/C] GTCTCCGTTCGCGCCAGTAC GCGCCAGTACCGCCGGTTAC [G/A] ATCTTAATGCCTTCACGTTC CGGTACTGCGAAAGCTGGAG [C/G] ATCAACTTGGAATTCCACAA AATCTTTGCCATTGCTGTCA [A/G] TATCTTCGTCAGCTTCAGCT GACAACGCTGGTGTATTGC [C/T] GAAATGGCTGGAATGAGCCA ATGCTCAGCACCATCGCCAC [T/C] GGTTTGGCGATTGATGCTTA AAACCAGGGTCCTTGATGTG [T/] GTCTACAACGCTTCCAACAA AAAAGTGCTATTGTTCAGGT [G] GATGCTGCTCCGTTCAAGCA TTGGGTATCTACGGACTGAT [C] ATCGCTGTTATCATCAGTAC GCGCCAGTACCGCCGGTTAC [A] ATCTCACTGCCTTCACGTCC CACTITICITICGIGGCTAAAT [T] CITICGGCCGAGCCGGTCTCA GTTATCATCAGTACCGGTAT [T] AACCCCAAGGCTAATTCTTA 29-N1/10E12/N2-2 28-N1/10E12/N2-1 41-85/11D4/86-2 33-85/10F9/N1-2 45-85/11D11/86 46-N2/11E3/N8a 43-N2/11D11/N3 44-86/11D11/N3 38-85/10F12/86 39-85/11B7/86 34-85/10F9/86 36-85/10H6/86 40-85/11C4/86 30-N1/10F4/N2 32-85/10F4/N2 23-85/10B9/86 35-86/10F12 25-10C8/N2 27-85/10D2 31-10F4/N2 24-10C8/N2 26-10D2/N1

7374

AATGCTTGTGGAGATtTACA [G/A] GTCCATACTGATGGCGCAGG

47-86/11E3/N2a

rage 3		
48-86/11E3/N2b	AATGCTTGTGGAGATCTACA [G/A] GTCCATACTGATGGCGCAGG	7475
49-85/11F12/86	AATGATTGGTTTGAGAAGCA [T/A] ACAGCTGGTACGCTTGATAT	7576
50-85/11F7/86	GATAGGGCGAAGAGGGAA [G/A] AGTCCTGAGAGAAAGAGAT	££9 <u>7</u>
51-85/11H2/86-2	CTCTCTCTCCACAAAGACAC [A/C] GCTTTCTCCATGACCTTCGG	<u>8±77</u>
52-85/11H5/86-2	TCTCTGACGTCATGAAAGCT[C/A]ATGGCAAAATTGCTGATGGA	· 6±8L
53-85/11H6/86-1a	GTTATCGATCGCGTGGTCCG [T/C] GAAACCCAAAATaCACCTTT	7980
54-85/11H6/86-1b	GTTATCGATCGCGTGGTCCG [T/C] GAAACCCAAAATtCACCTTT	808+
55-85/12B6/N3	CGTCAGCCTTCTTCCGCCGC [A/C] GTCGTCCTCCGCAACCGTGC	8182
56-86/12B6/85a	TGTCTCTTCCGTCAGCCTTC[C/T]TCCGCCGCAGTCGTCCTCCG	8283
57-86/12B6/85b	TGICTCTICCGICAGCCTIC [C/I] ICCGCCGCGGTCGICCTCCG	8384
58-86/12B11/85	TCAGGTTTACCTCTATATAT [T/]ATATTTCATGGTATGAAGGT	8485
59-n1/12B11/N2-2	TATCCTGCAAATTGACATTT [T/C] CCTTCAGGTTCTAGAAGCTG	<u>8586</u>
60-85/12C2/86	CGAGAACAGAAGAAGAGA [C/] TGGAACACGTCGGACAGTAC	<u>8687</u>
62-12C11/N2	ACGGGTCCTAGCGCCATGGC[T]ATTTTCCTCACCGTTTCTGG	88788
63-N1/12D10	TTGGGCTTTCGGTGGTATGA [T] CTTCGTCCTCGTCTATTGCA	6888
65-85/12F4/86-1	TCCTTGATTCCTTAATAATC [A/T] TTGGCTGGGGGTCTTTCTAA	0668
66-12G5/N1	GCTTGAATAACGATGTCTAC [T] CTGCCTCGGCGTACGGCGGA	<u>90</u> 94
67-85/12G8	CTAAAAAGATCGACGAGTGT [C] CCTTACTACGCTCCATCTAT	<u>91</u> 92
68-12G9/N1-1	AGGTGGGTTTAGCGTGGCAT[C]CGATCCATTGGATGGATCCA	9293
69-85/12G9/	NGTGGGTTTACCGTATCATT[T]GATCCATTGGATGGATCGAG	9394
70-12B11/N2-1	GCGGATCCTATATTGGGTCT [T] GATGGATTGTTTCTATCCCG	9495

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96 <u>56</u>	<u>£696</u>	9798	6686	99100	100101	101 102	102103	<u>103</u> 104	<u>104105</u>	105106	106107	107108	108109	109110	110111	1111112	<del>211</del> 2113
TATCCTGCAAATTGACATTT[C]CCTTCAGGTTCTAGAAGCTG	TACCACGGTCGTACTGGTCG [A] TGTCTGGAACGTCACCAAGC	CTGTCTCAGTTTGTTGGATC[C/G] AAATCGAATCGAAAGCGTAC	CTGTCTCAGTTTGGATC [C/G] AAATCAAATCGAAAGCGTAC	ACACTGTTGGAGGACGTGAA [G] AAGATATTCAAGACAACATC	TCTTTCGTATCTTGCTGAGT [C/T] GTTACGCCTGTCAACACCCG	GGAACCCTAGGGAGCCCACA [G] CTCCTTATGCTAAGCGGCGT	GATCATAGTATCCGCCGGAA[C]CCTAGGGAGCCCACAGCTCC	TTCGGCGGGTCGATCCGGGC [A/G] GAAGACATTGTCAGGTGANN	GCACCAACATTGTAAACCTA[T/G]AGCTTCTTCCTCAGCCACCT	GCTGCCACATAGTGAACCTA [T/A] AGCTTCTTCCTCAGCCACCT	GCACCAACATTGTGAACCTA [G/A] AGCTTCTTCCTCAGCCACCT	AGTACATAGCTATTGACTAA [C/G] TTAAGTTCCTTGTATTGTTG	CCTCTATCCGCCATGGTTGC [A/T] CCAACATTGTGAACCTAGAG	TTGACCCTCGGCAAGCCACC [G/T] GTCAAGCCATGCTGCAGCCT	AGGCTGCCCTCTCCCAATTC [A/C] AAAGCCAACTCCTAAACCAA	AAACATGGAAAGGCCTGATA [/G]TCACCGTCAAGCTCACCGTC	CAACCTGAAAATTGTTTTA [C/A] CAACGGCCCCGCTTTCTCCA
71-/12B11/N2-2	72-N1/12E10	73-N1/13A3/N2a	74-N1/13A3/N2b	75-13E8/N2	76-N1/13F6/N2-2	77-13F8/N2-1	78-13F8/N2	79-85/14B5/86	80-N1/14C2/N2	81-85/14C2/86-1	82-N2/14C2/85-2	83-85/14C2/86-2	84-N2/14C2/85-1	85-85/14E2/86-2	86-85/14E2/86-1	87-85/14E8/86	88-85/14E12/86

115446

114115

TCACCGGCTTGAAGTCTTCC [G/T] CTGCATTCCCAGTCACCCGC

90-85/14H10/86

89-14H10/86

91-85/15A6/86

AAGGCCAACAACGACATTAC [C] TCCATCGTTAGCAACGGAGG

ACTCAGCTTTCTTATGCCTC [G/] ACTTGCGACACACGAATCCA

113114

93-85/15E5/86-1 CGAGG/ 94-N1/15E5/N2-1 CTGTtC 95-N1/15E5/N2-2 CCC 96-86/15E5/N2 CCCGCC	ATCACTTCTCTGT [G/T] CAAGAAGAAGTTCGGCAAGG	117118
CT CT		011/11
5-N1/15E5/N2-2 96-86/15E5/N2 CC 97-15E9/86 TC	CAAGAAGAAGTTCGG [C/T] AAGGTCTACGCTTCCCGCGA	118419
	CCCTCTGCTCGTCACGGCGT [T/A] ACGCAGTTCTCGGATCTGAC	119120
	CCCGCGAGGAGCACGACTAC [A/T] GATTCTCCGTTTTCAAATCC	120121
	TCCACTCGCCGGGAAGAAC[T]CGACAAACCGTTGTCTACTT	121422
98-N2/15E9 ATGGCT	ATGGCTCGCGACGGGTCTCC [G] GTAAACCTCGGAGAGCAGAT	122123
99-N2/15E9/86 GCCGAC	GCCGACTCTCGAAGCTTCTT [A/] ACTCCACTCGCCGGGAAGAA	123124
100-85/15E9/86-1 GAA	GAATCTAGGAGAGCAGATCT [T/G] CCTCTCTATCTTCAATGTTC	124125
101-85/15E9/86-2 TCC	TCCACTCGCCGGGAAGAAC [C/T] CGACAAACCGTTGTCTACAT	125126
102-N1/15E9/N2-1 GTC	GTCATGAAGATATTCACTAC [A/G] CCGACTCTCGAAGCTTCTTA	126127
103-85/15F1/86 GCAGG	GCAGGTAAAATTCTACAGAC [C/A] TTCCCTTTTCATTGTAGTTA	<u>127</u> 128
104-85/15F5/86 TCT	TCTCCTCCGCGCGCAAGAA [G/A] AAATCGACAGCGGCGCGTCT	128
105-85/15F10/86 GTG	SCCCTAAAGATACCCTCA [A/G] GCTTGGTGTCTGCGCTAATG	129
106-N2/15G1 TTCTT	TTCTTCCCACAGGTGAAACT [T]GCTAACTTCCTTCCAAAGTA	130
107-N1/15H7/N2 TATG	STATCAGGACAATGTGT [GA/TT] GTGACTGTGGTTGCATCCAT	131
108-N1/16A1/N2-1 GCTAAC	GCTAAGCTACGCAACTGCCA [C/T] CAATCAGGGCAAGCTAAAGG	132
109-85/16A5/86 TATAC?	TATACACTCTTTAAAAGCGT [G/C] TGTGTGTACCCATCTCTTT	133
110-N1/16B6/N2 ATGGCT	ATGGCTGCGTATTGGCTGTC [C/T] AAGGCTGGATCTTGGTCCCA	134
111-85/16B6/N1 GGATC	GGATCCATCTCAACTATGGT [A/C] GTATTATCGTTGAGGCTAGG	135
112-85/16B7/86 GTA	ATGTGATTCGGAAGAA [T/] CAAACTAAGTGCCGAGAAAG	136
113-N1/16D6/N2 GCTAAG	GCTAAGGTAGTTGGAGGAGC [CAA/GTG] CCACAGCCACGCGACTAAGG	137
114-85/16D10/86 CTCAA	CTCAACGTAGCAAGTAATAA [T/G]ATACTGTCTATTTATGGTTA	138

139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160
AGACTTTCCCCATTCTCTTC [T/A] CCATCCACCGTCGAAACCCA	ACTTCGAAACTGTAAACCTA [A/T] ACTTTAAGAGTTTAGAGCTA	CACCATCGGAGAAAGAGGTA[C/T]TTCGAAACTGTAAACCTAAA	CTAAGGCGTCTCCTGAAGAA [A/G] TACAGAGAGTCGAAGAAGAT	CCGCGGACGACGCTTTCTTC [C/A] TCTGCTCCACCGCGAGCGCC	GAGGAGTAGTCTCCATGGCC [G/] AAGAAGAGCGTCGGAGACCTG	GAAGTTAGGGCTTCTAAGAT[C/T]AAGTTCGGCAAGGCTTTAAC	TCAAAACTAATATTTCTTTT [G/C] TTGATTGGTAATAAACAGGT	TTCCAGTGAAAAGGCATTGT [T/G] CTCCAAAATCTCGCTCTGCG	AAGCAGCTCTGACTTGAATG [C/A] GAGAGGTTAATCAGACTGTG	TAGATTGAAGCAATCAAGAA [G/A] ATCTCAGACTTCATCACCCA	GCATCCAACTCCAAGGATGA [/C] CCTGCCAAGGTGCTGCTAACT	GAGCTCAGGGATGGTGGATC [A/T] GACTACCTTGGAAAGGGTGT	TGGGGTTAGTCGAAATAGGT [A/T] AAATGCTTTGAGTATGTGTA	TACGCGCAGCACGGACTTGC [G/A] ACGCAAGCAATCGAGCTTTT	GAAGCCCATGGTACGGAGCG [G/A] GAGAGAGTCAAGTACTTGGG	AACGGGTCACTGCTAAATCA [T/A] AAGGATCACAAGGCTGGGAC	CTAGCCTACTTTGGGAAAAG [/T] TTCGTTATTGTTTTGTGTGG	GACTTCAAGGACTTCGCCGG [A/C] AAATGCTCCGACGCTGTCAA	GAGGAGGCTACATGCAGCT [G/A] AAGAGGCTGAGGGGGCTAAA	GATGTTCAACCTATGAAGAA [G/C] AAACACCGAGGACCAACGAG	CCATTAGTGAGGGAGCATGT [T/A] CCTGTCACATTTGATGATTG
115-N1/16E9/N2 P	116-85/16H3/86-1 F	117-85/16H3/86-2 C	118-85/17A5/86	119-85/17C7/86	120-85/17F7/86	121-85/17G12/86	122-85/18A2/86	123-85/18A11/86	124-85/18F5/86   P	125-85/18H10/86-3	126-85/19B3/86	127-85/19C8/86 C	128-N1/19F4/N2	129-N1/19H1/N2	130-85/20B4/86-1 C	131-N1/20B12/N2 A	132-85/20C12/86 (	133-85/20D2/86	134-85/20D3/86-2	135-85/20D6/86-4	136-85/20D6/86-5 (

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161	162	163	164	165	166	167	168	169	170	171	172	173
AAACACATCGCCAAAGATCC [CG/AA] ACACTCGAGAAAGAGTGGAG	CTCATAGGCGATCTGGAGTA [T/G] GCAAATCGAATCTCCTCCC	TGCACGCCTCACTTGTTCCT[T/A]CCAATCTGACATCAAGGATT	NGTGTTTTTGAGGTGAAAGC [A/T] ACAAATGGAGATACCTTTTT	CCCGAGCCATTAGGACAAGA[T/C]GACTTGCCGTTTGACCAAAC	CCCATCTCATCCTTGA [A/G] CCGTTGAATCAAGCTCCTGG	TACATTCTCATTGGTTGGTT[C/A]TTGGGAAATAAAGTACCAAC	GCACGCGCTAGAGTTGTTGC [C] AGAAGGAATGAACAATCTGA	CTTGAGACCTATAGTCCTGT [A/T] GTTCGGTCCGCCACAGTTCG	CACAGTTCGTACAGTTCTTC [A/C] CATTGCCACTGTTATGCACT	GAAGGCGTCCACTATCTTGA [A/G] ACCTATAGTCCTGTTGTTCG	TCCCGGAAATCTTGCTGAAA[A/C]CGTTTACCTGCGACAACCAG	ATGTCTTCAAAGTGCTCTGT [T] GCAACGCACGTCCGAACAAG
137-85/20D6/86-8	138-N1/20D8/N2	139-N1/20E1/N2	140-N1/20F1/N2-1	141-N1/BoC-a2/N3-2	142-N1/BOC-A2/N3-1	143-N1/BoC-a2/N3-3	144-86/SC3	145-N3/SC3/N4-1	146-N3/SC3/N5-1	147-N1/SC3/N3-1	148-86/SC3/N4-1	149-B11/N5-1